

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/632,098

DATE: 08/17/2000
TIME: 10:48:16

Input Set : A:\9939.SEQ.txt
Output Set: N:\CRF3\08162000\I632098.raw

4 <110> APPLICANT: Sheppard, Paul O.
5 Baindur, Nand
6 Bishop, Paul D.
8 <120> TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
10 <130> FILE REFERENCE: 99-39
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/632,098
C--> 12 <141> CURRENT FILING DATE: 2000-08-02
12 <160> NUMBER OF SEQ ID NOS: 26
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 3431
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (37)...(2442)
25 <400> SEQUENCE: 1
26 gcgagccgct gcctagaggc cgaggagctc acagct atg ggc tgg agg ccc cgg 54
27 Met Gly Trp Arg Pro Arg
28 1 5
30 aga gct cgg ggg acc ccg ttg ctg ctg ctg cta ctg ctg ctg ctc 102
31 Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu
32 10 15 20
34 tgg cca gtg cca ggc gcc ggg gtg ctt caa gga cat atc cct ggg cag 150
35 Trp Pro Val Pro Gly Ala Gly Val Leu Gln Gly His Ile Pro Gly Gln
36 25 30 35
38 cca gtc acc ccg cac tgg gtc ctg gat gga caa ccc tgg cgc acc gtc 198
39 Pro Val Thr Pro His Trp Val Leu Asp Gly Gln Pro Trp Arg Thr Val
40 40 45 50
43 agc ctg gag gag ccg gtc tcg aag cca gac atg ggg ctg gtg gcc ctg 246
44 Ser Leu Glu Glu Pro Val Ser Lys Pro Asp Met Gly Leu Val Ala Leu
45 55 60 65 70
47 gag gct gaa ggc cag gag ctg ctt gag ctg gag aag aac cac agg 294
48 Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu Leu Lys Asn His Arg
49 75 80 85
51 ctg ctg gcc cca gga tac ata gaa acc cac tac ggc cca gat ggg cag 342
52 Leu Leu Ala Pro Gly Tyr Ile Glu Thr His Tyr Gly Pro Asp Gly Gln
53 90 95 100
55 cca gtg gtg ctg gcc ccc aac cac acg gat cat tgc cac tac caa ggg 390
56 Pro Val Val Leu Ala Pro Asn His Thr Asp His Cys His Tyr Gln Gly
57 105 110 115
59 cga gta agg ggc ttc ccc gac tcc tgg gta gtc ctc tgc acc tgc tct 438
60 Arg Val Arg Gly Phe Pro Asp Ser Trp Val Val Leu Cys Thr Cys Ser
61 120 125 130
63 ggg atg agt ggc ctg atc acc ctc agc agg aat gcc agc tat tat ctg 486
64 Gly Met Ser Gly Leu Ile Thr Leu Ser Arg Asn Ala Ser Tyr Tyr Leu
65 135 140 145 150

ENTERED

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67	cgt ccc tgg cca ccc cgg ggc tcc aag gac ttc tca acc cac gag atc	534
68	Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp Phe Ser Thr His Glu Ile	
69	155 160 165	
71	ttt cgg atg gag cag ctg ctc acc tgg aaa gga acc tgt ggc cac agg	582
72	Phe Arg Met Glu Gln Leu Leu Thr Trp Lys Gly Thr Cys Gly His Arg	
73	170 175 180	
75	gat cct ggg aac aaa gcg ggc atg acc agc ctt cct ggt ggt ccc cag	630
76	Asp Pro Gly Asn Lys Ala Gly Met Thr Ser Leu Pro Gly Gly Pro Gln	
77	185 190 195	
79	agc agg ggc agg cga gaa gcg cgc agg acc cgg aag tac ctg gaa ctg	678
80	Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr Arg Lys Tyr Leu Glu Leu	
81	200 205 210	
83	tac att gtg gca gac cac acc ctg ttc ttg act cgg cac cga aac ttg	726
84	Tyr Ile Val Ala Asp His Thr Leu Phe Leu Thr Arg His Arg Asn Leu	
85	215 220 225 230	
87	aac cac acc aaa cag cgt ctc ctg gaa gtc gcc aac tac gtg gac cag	774
88	Asn His Thr Lys Gln Arg Leu Leu Glu Val Ala Asn Tyr Val Asp Gln	
89	235 240 245	
91	ctt ctc agg act ctg gac att cag gtg gcg ctg acc ggc ctg gag gtg	822
92	Leu Leu Arg Thr Leu Asp Ile Gln Val Ala Leu Thr Gly Leu Glu Val	
93	250 255 260	
95	tgg acc gag cgg gac cgc agc cgc gtc acg cag gac gcc aac gcc acg	870
96	Trp Thr Glu Arg Asp Arg Ser Arg Val Thr Gln Asp Ala Asn Ala Thr	
97	265 270 275	
99	ctc tgg gcc ttc ctg cag tgg cgc cgg ggg ctg tgg gcg cag cgg ccc	918
100	Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly Leu Trp Ala Gln Arg Pro	
101	280 285 290	
103	cac gac tcc gcg cag ctg ctc acg ggc cgc gcc ttc cag ggc gcc aca	966
104	His Asp Ser Ala Gln Leu Leu Thr Gly Arg Ala Phe Gln Gly Ala Thr	
105	295 300 305 310	
107	gtg ggc ctg gcg ccc gtc gag ggc atg tgc cgc gcc gag agc tgc gga	1014
108	Val Gly Leu Ala Pro Val Glu Gly Met Cys Arg Ala Glu Ser Ser Gly	
109	315 320 325	
111	ggc gtg agc acg gac cac tgc gag ctc ccc atc ggc gcc gca gcc acc	1062
112	Gly Val Ser Thr Asp His Ser Glu Leu Pro Ile Gly Ala Ala Ala Thr	
113	330 335 340	
115	atg gcc cat gag atc ggc cac agc ctc ggc ctc agc cac gac ccc gac	1110
116	Met Ala His Glu Ile Gly His Ser Leu Gly Leu Ser His Asp Pro Asp	
117	345 350 355	
119	ggc tgc tgc gtg gag gct gcg gcc gag tcc gga ggc tgc gtc atg gct	1158
120	Gly Cys Cys Val Glu Ala Ala Ala Glu Ser Gly Gly Cys Val Met Ala	
121	360 365 370	
123	gcg gcc acc ggg cac ccg ttt ccg cgc gtg ttc agc gcc tgc agc cgc	1206
124	Ala Ala Thr Gly His Pro Phe Pro Arg Val Phe Ser Ala Cys Ser Arg	
125	375 380 385 390	
128	cgc cag ctg cgc gcc ttc ttc cgc aag ggg ggc ggc gct tgc ctc tcc	1254
129	Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly Gly Ala Cys Leu Ser	
130	395 400 405	
132	aat gcc ccg gac ccc gga ctc ccg gtg ccg ccg gcg ctc tgc ggg aac	1302

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133	Asn	Ala	Pro	Asp	Pro	Gly	Leu	Pro	Val	Pro	Pro	Ala	Leu	Cys	Gly	Asn	
134				410					415					420			
136	ggc	ttc	gtg	gaa	gcg	ggc	gag	gag	tgt	gac	tgc	ggc	cct	ggc	cag	gag	1350
137	Gly	Phe	Val	Glu	Ala	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Pro	Gly	Gln	Glu	
138				425					430					435			
140	tgc	cgc	gac	ctc	tgc	tgc	ttt	gct	cac	aac	tgc	tcg	ctg	cgc	ccg	ggg	1398
141	Cys	Arg	Asp	Leu	Cys	Cys	Phe	Ala	His	Asn	Cys	Ser	Leu	Arg	Pro	Gly	
142				440					445					450			
144	gcc	cag	tgc	gcc	cac	ggg	gac	tgc	tgc	gtg	cgc	tgc	ctg	ctg	aag	ccg	1446
145	Ala	Gln	Cys	Ala	His	Gly	Asp	Cys	Cys	Val	Arg	Cys	Leu	Leu	Lys	Pro	
146				455					460					465		470	
148	gct	gga	gcg	ctg	tgc	cgc	cag	gcc	atg	ggg	gac	tgt	gac	ctc	cct	gag	1494
149	Ala	Gly	Ala	Leu	Cys	Arg	Gln	Ala	Met	Gly	Asp	Cys	Asp	Leu	Pro	Glu	
150				475					480					485			
152	ttt	tgc	acg	ggc	acc	tcc	tcc	cac	tgt	ccc	cca	gac	gtt	tac	cta	ctg	1542
153	Phe	Cys	Thr	Gly	Thr	Ser	Ser	His	Cys	Pro	Pro	Asp	Val	Tyr	Leu	Leu	
154				490					495					500			
156	gac	ggc	tca	ccc	tgt	gcc	agg	ggc	agt	ggc	tac	tgc	tgg	gat	ggc	gca	1590
157	Asp	Gly	Ser	Pro	Cys	Ala	Arg	Gly	Ser	Gly	Tyr	Cys	Trp	Asp	Gly	Ala	
158				505					510					515			
160	tgt	ccc	acg	ctg	gag	cag	cag	tgc	cag	cag	ctc	tgg	ggg	cct	ggc	tcc	1638
161	Cys	Pro	Thr	Leu	Glu	Gln	Gln	Cys	Gln	Gln	Leu	Trp	Gly	Pro	Gly	Ser	
162				520					525					530			
164	cac	cca	gct	ccc	gag	gcc	tgt	ttc	cag	gtg	gtg	aac	tct	gcg	gga	gat	1686
165	His	Pro	Ala	Pro	Glu	Ala	Cys	Phe	Gln	Val	Val	Asn	Ser	Ala	Gly	Asp	
166				535					540					545		550	
168	gct	cat	gga	aac	tgc	ggc	cag	gac	agc	gag	ggc	cac	ttc	ctg	ccc	tgt	1734
169	Ala	His	Gly	Asn	Cys	Gly	Gln	Asp	Ser	Glu	Gly	His	Phe	Leu	Pro	Cys	
170				555					560					565			
172	gca	ggg	agg	gat	gcc	ctg	tgt	ggg	aag	ctg	cag	tgc	cag	ggg	gga	aag	1782
173	Ala	Gly	Arg	Asp	Ala	Leu	Cys	Gly	Lys	Leu	Gln	Cys	Gln	Gly	Gly	Lys	
174				570					575					580			
176	ccc	agc	ctg	ctc	gca	ccg	cac	atg	gtg	cca	gtg	gac	tct	acc	gtt	cac	1830
177	Pro	Ser	Leu	Leu	Ala	Pro	His	Met	Val	Pro	Val	Asp	Ser	Thr	Val	His	
178				585					590					595			
180	cta	gat	ggc	cag	gaa	gtg	act	tgt	cgg	gga	gcc	ttg	gca	ctc	ccc	agt	1878
181	Leu	Asp	Gly	Gln	Glu	Val	Thr	Cys	Arg	Gly	Ala	Leu	Ala	Leu	Pro	Ser	
182				600					605					610			
184	gcc	cag	ctg	gac	ctg	ctt	ggc	ctg	ggc	ctg	gta	gag	cca	ggc	acc	cag	1926
185	Ala	Gln	Leu	Asp	Leu	Gly	Leu	Gly	Leu	Val	Glu	Pro	Gly	Thr	Gln		
186				615					620					625		630	
188	tgt	gga	cct	aga	atg	gtg	tgc	cag	agc	agg	cgc	tgc	agg	aag	aat	gcc	1974
189	Cys	Gly	Pro	Arg	Met	Val	Cys	Gln	Ser	Arg	Arg	Cys	Arg	Lys	Asn	Ala	
190				635					640					645			
192	ttc	cag	gag	ctt	cag	cgc	tgc	ctg	act	gcc	tgc	cac	agc	cac	ggg	gct	2022
193	Phe	Gln	Glu	Leu	Gln	Arg	Cys	Leu	Thr	Ala	Cys	His	Ser	His	Gly	Ala	
194				650					655					660			
196	ggg	ctc	cac	cct	tct	gtg	aca	agc	cag	gct	ttg	gtg	gca	gca	tgg	aca	2070
197	Gly	Leu	His	Pro	Ser	Val	Thr	Ser	Gln	Ala	Leu	Val	Ala	Ala	Trp	Thr	

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198          665          670          675
200  gtg gcc ctg tgc agg ctg aaa acc atg aca cct tcc tgc tgg cca tgc      2118
201  Val Ala Leu Cys Arg Leu Lys Thr Met Thr Pro Ser Cys Trp Pro Cys
202          680          685          690
204  tcc tca gcg tcc tgc tgc ctc tgc tcc cag ggg ccg gcc tgg cct ggt      2166
205  Ser Ser Ala Ser Cys Cys Leu Cys Ser Gln Gly Pro Ala Trp Pro Gly
206  695          700          705          710
208  gtt gct acc gac tcc cag gag ccc atc tgc agc gat gca gct ggg gct      2214
209  Val Ala Thr Asp Ser Gln Glu Pro Ile Cys Ser Asp Ala Ala Gly Ala
210          715          720          725
213  gca gaa ggg acc ctg cgt gca gtg gcc cca aag atg gcc cac aca ggg      2262
214  Ala Glu Gly Thr Leu Arg Ala Val Ala Pro Lys Met Ala His Thr Gly
215          730          735          740
217  acc acc ccc tgg gcg gcg ttc acc cca tgg agt tgg gcc cca cag cca      2310
218  Thr Thr Pro Trp Ala Ala Phe Thr Pro Trp Ser Trp Ala Pro Gln Pro
219          745          750          755
221  ctg gac agc cct ggc ccc tgg acc ctg aga act ctc atg agc cca gca      2358
222  Leu Asp Ser Pro Gly Pro Trp Thr Leu Arg Thr Leu Met Ser Pro Ala
223          760          765          770
225  gcc acc ctg aga agc ctc tgc cag cag tct cgc ctg acc ccc aag atc      2406
226  Ala Thr Leu Arg Ser Leu Cys Gln Gln Ser Arg Leu Thr Pro Lys Ile
227  775          780          785          790
229  aag tcc aga tgc caa gat cct gcc tct ggt gag agg tagctcctaa      2452
230  Lys Ser Arg Cys Gln Asp Pro Ala Ser Gly Glu Arg
231          795          800
233  aatgaacaga tttaaagaca ggtggccact gacagccact ccaggaactt gaactgcagg      2512
234  ggcagagcca gtgaatcacc ggacctccag cacctgcagg cagcttgaa gttcttccc      2572
235  cgagtggagc ttcgacccac ccactccagg aaccagagc cacattagaa gttcctgagg      2632
236  gctggagAAC actgctgggc aactctcca gctcaataaa ccatcagtc cagaagcaaa      2692
237  ggtcacacag cccctgacct ccctcaccag tggaggettg gtagtgctgg ccacccaaa      2752
238  agggctctgt cctgggagtc tgggtgtgt cctacatgca atttcacgg acccagctct      2812
239  gtggagggca tgactgctgg ccagaagcta gtggtcctgg ggcctatgg ttcgactgag      2872
240  tccacactcc cctggagcct ggctggcctc tgcaaaacaaa cataattttg gggaccttcc      2932
241  ttctgttttc ttcccacct gtcttctccc ctagggtggt cctgagcccc caccaccaat      2992
242  cccagtgcta cactgaggt tctggagctc agaattctgac agcctctccc ccattctgtg      3052
243  tgtgtcgggg ggacagaggg aaccatttaa gaaaagatac caaagtagaa gtcaaaagaa      3112
244  agacatgttg gctataggcg tgggtggctca tgcctataat ccagcactt tgggaagccg      3172
245  gggtaggagg atcaccagag gccagcaggt ccacaccagc ctgggcaaca cagcaagaca      3232
246  cgcactctac agaaaaattt taaaattagc tgggcgtggg ggtgtgtacc ttagggccta      3292
247  gctgctcagg aggctgaagc aggaggatca cttgagcctg agttcaacac tgcagtgagc      3352
248  tatgggtggc ccactgcact ccagcctggg tgacagagca agaccctgtc tctaaaataa      3412
249  attttaaaaa gacatatta
251 <210> SEQ ID NO: 2
252 <211> LENGTH: 802
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 2
257 Met Gly Trp Arg Pro Arg Arg Ala Arg Gly Thr Pro Leu Leu Leu Leu
258 1 5 10 15

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```

259 Leu Leu Leu Leu Leu Leu Trp Pro Val Pro Gly Ala Gly Val Leu Gln
260      20      25      30
261 Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly
262      35      40      45
263 Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp
264      50      55      60
265 Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu
266      65      70      75      80
267 Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His
268      85      90      95
269 Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp
270      100     105     110
271 His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val
272      115     120     125
273 Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg
274      130     135     140
275 Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp
276      145     150     155     160
277 Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys
278      165     170     175
279 Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser
280      180     185     190
281 Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr
282      195     200     205
283 Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu
284      210     215     220
285 Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val
286      225     230     235     240
287 Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala
288      245     250     255
289 Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr
290      260     265     270
291 Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly
292      275     280     285
293 Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg
294      290     295     300
295 Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys
296      305     310     315     320
297 Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro
298      325     330     335
299 Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly
300      340     345     350
301 Leu Ser His Asp Pro Asp Gly Cys Val Glu Ala Ala Ala Glu Ser
302      355     360     365
303 Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val
304      370     375     380
305 Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly
306      385     390     395     400
307 Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:739 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:748 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

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L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6